

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: August 23, 2003, 20:43:40 ; Search time 1898 Seconds

(without alignments)
4481.858 Million cell updates/sec

SUMMARIES

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Title: US-09-745-506-37
Perfect score: 350
Sequence: 1 MDKALLSLNDPFLSPFAE.....LEKNITLSEDRDPIQVY 350

Scoring table:
OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Word size: 1

Total number of hits satisfying chosen parameters: 45562604

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL-frame.p2n.model -DEV-xlh
-o-/cgn2_1/USPTO/US09745506/runat_22082003_104428_7276/app_query.fasta_1.519
-DB-EST -QFMT-fastap -SUFIX-p2noli.rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-ONITS-bits -START=1 -END=1 -MATRIX=oligo -TRANS-human40.cdi -List=45
-LOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc
-NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09745506.GC6N1.1.2135 &runat_22082003_104428_7276 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEBUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMECUT=120 -WARN_TIMECUT=30 -THREDS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estlin:*

4: em_estlmu:*

5: em_estlov:*

6: em_estlpl:*

7: em_estro:*

8: em_hlc:*

9: gb_est1:*

10: gb_est2:*

11: gb_hlc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estlum:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_dln:*

20: em_gss_vrt:*

21: em_gss_vrt:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

Result No.	Score	Query Match	Length	DB ID	Description
1	286	81.7	1201	13	BX446370
2	275	78.6	1201	9	AL581997
3	267	76.3	987	13	BUI72435
4	267	76.3	930	13	BX393871
5	256	73.1	836	13	BQ229243
6	243	69.4	957	9	AL521920
7	242	69.1	1117	12	BM45164
8	237	67.7	890	9	AL520538
9	221	63.1	1019	12	BM557530
10	216	61.7	1201	9	AL529615
11	214	61.1	877	13	BQ437698
12	214	61.1	929	13	BUI755123
13	213	60.9	759	10	BE275324
14	211	60.3	817	12	BI755123
15	210	60.0	1201	13	BX377118
16	208	59.4	843	13	BUI755123
17	208	59.4	980	13	BUI755123
18	203	58.0	963	10	BE797115
19	202	57.7	859	10	BE797115
20	201	57.4	945	10	BE747311
21	198	56.6	958	10	BE797115
22	197	56.3	845	10	BE797115
23	194	55.4	728	14	CD102399
24	189	54.0	568	14	CD122465
25	189	54.0	732	10	BE797115
26	189	54.0	1031	13	BX385102
27	185	52.9	600	14	CB146277
28	183	52.3	549	12	BM712181
29	180	51.4	638	14	CB122989
30	180	51.4	909	13	BUI755123
31	177	50.6	1074	13	BX339176
32	177	50.6	1119	10	BE745052
33	174	49.7	610	12	BM41141
34	174	49.7	920	10	BE696536
35	173	49.4	742	12	BI093955
36	172	49.1	666	13	BUI755123
37	172	49.1	888	13	BUI755123
38	170	48.6	562	12	BM42929
39	164	46.9	865	10	BE727240
40	162	46.3	753	10	AM957667
41	161	46.0	905	10	BE797115
42	161	46.0	1032	12	BM810545
43	161	46.0	1201	9	AL582089
44	159	45.4	628	10	BF034644
45	157	44.9	472	14	CB142204

ALIGNMENTS

RESULT 1
BX446370
LOCUS
DEFINITION BX446370 Homo sapiens PLACENTA Homo sapiens CDNA clone CIOBA00442B11
ACCESSION BX446370
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 1201)

Db 303 CTGAATTGCTACGAGAGGCTTTGATGACGAGGTGTAGATTTTCTTCCCGGAACAAACA 362
QY 204 LeuTyrGlnYsrThrGlnIleLeuSerLeuGlnYsrProLeuLeuHisThrGlyMet 223
363 CTTTATCAGAGAGAGGAAATTCGTCTACGTGAGAGAGCTTGGTCTTACATACGAGATG 422
QY 224 GLYArgLeuGlnYsrThrLeuAspGlnSerValSerLeuAlaThrMetIleAspAlaGly 243
423 GGAAGGTTATGACACACGATGATGATCTCTCCCTGGCAACATGATGATGATGATGATG 482
QY 244 ArgHisLeuYsrLeuSerHisIleArgLeuAlaLeuGlnYsrValGlyArgThrLeuGlnSer 263
483 AGACACCTAAAGATCATCTCATATTCCTTACCTTGGGAGGAGAAACCTTATGATGCT 542
QY 264 GlnValYsrValAlaLeuGlnYsrValGlySerGlySerValLeuGlnYsrValGln 283
543 CAAGTCAAAAGTCCGCGCCCTGTGTGCTGTCTGGAGACGCTTCTGAGGGGTGTAG 602
QY 284 AlaAspLeuYsrLeuThrGlnYsrGlnMetSerHisAspThrLeuAspAlaIleSerGln 303
603 GCTGACCTTTTACCTCAGAGGATGATGATGATGATGATGATGATGATGATGATGATG 662
QY 304 GlnYsrValIleLeuGlnYsrGlnHisSerAspThrGlnArgGlyPheLeuSerAspLeu 323
663 GGAATTAATGCTCATCTCTCTGGAACACAGACACTGACAGAGCTTCTTCTGACCTT 722
QY 324 ArgAspMetLeuAspSerHisLeuGlnYsrIleAsnIleLeuSerGlnThrAsp 343
723 CGAGATATGCTGATCTCCTACTGAGATTAATTAATTAATTAATTAATTAATTAATTAAT 782
QY 344 ArgAspProLeuGlnValVal 350
783 AGGAGCCCTCTTCAGGTGTA 803

RESULT 4
LOCUS BX393871 930 bp mRNA linear EST 13-MAY-2003
DEFINITION BX393871 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
CDNA clone CS0DC0051M21 5-PRIME, mRNA sequence.
ACCESSION BX393871
VERSION BX393871.1 GI:30624084
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 930)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
JOURNAL Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1287.f for
more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bldn/cluster.cgl1seq-CS0DC0051M21P1cluster=1287.f. Contact :
Peng Jiang Email: fliang@lifetech.com URL: <http://fulllength.invitrogen.com/>
Paraday Avenue Genoscope sequence ID: CS0DC0051M21P1.
FEATURES
Source location/Qualifiers
1..930
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC0051M21"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V

BASE COUNT 248 a 231 c 214 g 237 t sites of the PCMVSPORT 6 vector. Library was normalized."
ORIGIN
Alignment Scores:
Pred. No.: 8,14e-249 Length: 930
Score: 267.00 Matches: 267
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 76.29% Indels: 0
DB: 13 Gaps: 0
US-09-745-506-37 (1-350) x BX393871 (1-930)
QY 1 MetAspLeuYsrAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGln 20
130 ATGATATTGAGAGGCTCTCCCTTCTCTCTTGAATGACTTTCATCCCTCTGCTTGGCTGAG 189
Db
QY 21 SerTrpAspAsnValGlyLeuLeuValGlnProSerProHisThrValAsnThrLeu 40
190 AGTGGGACATGTTGGATTACTGTGGAAACCAAGCCACACATCTGTAATACATC 249
Db
QY 41 PheLeuThrAsnAspLeuThrGlnGlnValMetGlnGlnValLeuGlnYsrValAsp 60
250 TTCTGACCAATGACCTGACGAGAGAGTGTGAGAGGAGTGTGCAAAAGGACAGAC 309
Db
QY 61 LeuIleLeuSerYsrHisProProIlePheArgProMetYsrAspGlyIleThrPheThr 80
310 CTCATTTCTCTCTCCATCCGCTTCCTTCCGACCCATGAAAGCGCAATACCTGGACACA 369
QY 81 TrpYsrGlnArgLeuValIleArgAlaLeuGlnYsrAsnArgValGlyIleYsrProHis 100
370 TGGAGAGAGCGCTGCTGATCCGGCTCTGGAGAACAGAGCGGTATCTACTCTCCAT 429
Db
QY 101 ThrAlaTrpAspAlaAlaProGlnGlnYsrAsnTrpLeuAlaYsrGlyLeuGlnYsrAla 120
430 ACAGCGTATGATGCTGCGCCCGCCAGGCGTCAACAACTGTTGGCTAAAGGGCTTGGAGCT 489
Db
QY 121 CysThrSerArgProIleHisProSerYsrAlaProAsnYsrProThrGlnYsrHis 140
490 TGTACCTCCAGGCCCATCATCATCTCCAAAGCTCCCAACTACCTTACAGAGAGGAAACCA 549
Db
QY 141 ArgValGlnPheAsnValAsnYsrThrGlnAspLeuAspYsrValMetSerAlaValYsr 160
550 CGAGTAGAATTCACACGTTTAATCTACACCAACCTGGACAAAGTCATGTCGAGTGA 609
Db
QY 161 GlnYsrAspGlnYsrValThrSerPheSerAlaArgThrGlnYsrGlnGlnYsrThr 180
610 GGAATTGACGGTGTTCGTGCACCTTCTCTGCTAGAGCTGTAATGAGAACAAACA 669
Db
QY 181 ArgIleAsnLeuAsnYsrThrGlnYsrAlaLeuMetGlnValValAspPheLeuSerArg 200
670 CGGATTAATTCGAAATTTGACTACAGAGAGCTTGTGATGCGGTGATGATTTCTTCCCGG 729
Db
QY 201 AsnYsrGlnLeuYsrGlnYsrThrGlnIleLeuSerLeuGlnYsrProLeuLeuHis 220
730 AACCAACACTTTTACAGAGAGAGGAAATTTGTGCATCGGAGAAACCTTCTCTTACTAT 789
Db
QY 221 ThrGlnMetGlnYsrGlnYsrThrLeuAspGlnSerValSerLeuAlaThrMetIleAsp 240
790 ACTGGAATGGAGACGGTTTATGACACACTGATGATGATGATGATGATGATGATGATGAT 849
Db
QY 241 ArgIleYsrArgHisLeuYsrLeuSerHisIleArgLeuAlaLeuGlnYsrValGlyArgThr 260
850 CGAATTAATAAAGACACTTAAATTAATCTATATGCTTATGCTTGGGCTTGGGAGAAC 909
Db
QY 261 LeuGlnYsrGlnValYsrVal 267
910 TTAGAGTCTCAAGTCAAGTC 930

RESULT 5
LOCUS BQ229243 836 bp mRNA linear EST 02-MAY-2002

```

DEFINITION  AGENCOURT_7510797 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6055296
5', mRNA sequence.
ACCESSION   BQ229243
VERSION     BQ229243.1 GI:20410643
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 836)
AUTHORS     NIH-MGC http://mgi.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgarbs-remail.nih.gov
            Tissue Procurement: ATCC/DCPD/OTF
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLM13315 row: f column: 01
            High quality sequence stop: 677.
            Location/Qualifiers
                1..836
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:6055296"
                /tissue_type="melanotic melanoma"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: skin; Vector: pCMV-SPORT6; Site:1: NotI;
                Site:2: SalI; Cloned unidirectionally. Primer: Oligo dt.
                Average insert size 2 kb. Library constructed by Life
                Technologies."
BASE COUNT   218 a 205 c 200 g 211 t 2 others
ORIGIN
Alignment Scores:
Prid. No.:      3,58e-238      length:      836
Score:          256.00         Matches:     256
Percent Similarity: 100.00%     Conservative: 0
Best Local Similarity: 73.14%   Mismatches: 0
Query Match:    13            Indels:      0
DB:              Gaps:        0

US-09-745-506-37 (1-350) x BQ229243 (1-836)
QY      3 LeuysAlaLeuLeuSerSerLeuAnaAspPheAlaSerLeuSerPheAlaGluSerTrp 22
Db      2 TTGAAGGCTCTCTCTCTCTCTCTGAATGAGCTTGCCTCCGTTCTCTGAGAGTTGG 61
QY      23 AspAsnValAlaGluLeuValAlaGluProSerProProHisThrValAsnThrLeuPheLeu 42
Db      62 GACATAGTGTGATCTAGTGTGAGACCAACCCACCATACATCTAAATACACTCTTCCG 121
QY      43 ThrAsnAspLeuThrGluGluValMetGluGluValLeuGluLysLysAlaAspLeuLe 62
Db      122 ACCAATGACCTGACGAGAGATGATGAGAGGCTCTCCAAAGAGAGACGACCTCAT 181
QY      63 LeuSerTyrHisProProIlePheArgPheMetLysArgTilleThrTrpAsnThrTrpLys 82
Db      182 CTCCTCTACCATCCGCTATCTTCCTCCAGACCATGAAACCGATTAACCTGGAACATGGAAG 241
QY      83 GluArgLeuValIleArgAlaLeuGluAsnArgValAlaGlyIleTyrSerProHisThrAla 102
Db      242 GAGCCGCTGTGATCTCGGCTCTGGAGAACAGAGTGGTATCTACTCTCTCTATACAGCC 301
QY      103 TyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAlaCysTrp 122
Db      302 TATGATGCTGCGCCCGAGGCGTCAACACACTGCTTGAAGGCGTGGAGCTTCTTACC 361

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QY      123 SerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHisArgVal 142
Db      362 TCCAGGCCCATATCATCTCTCCAAAGCTCCCACTACCTACAGAGGAAACCCAGTA 421
QY      143 GluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLysGlyIle 162
Db      422 GAATTCACAGTTATACATACACCCAGACCTGAGAACAGTATCTGCTCAGTGAAGAAAT 481
QY      163 AspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluInThrArgIle 182
Db      482 GAGCGGTCTCTCTCACTCTCTCTCTCTGCTGAGAGCTGTGTAATGAGAACAAACAGGATT 541
QY      183 AsnLeuAsnCysThrGlnLysAlaLeuMetGluValValAspPheLeuSerArgAsnLys 202
Db      542 AATCTAATATGATCTCAAGAAAGGCTTGATGACAGCTGTGATTTCTTCCCGAACAA 601
QY      203 GlnLeuTyrGlnLysThrGluLeuSerLeuGluLysProLeuLeuHisThrGly 222
Db      602 CAACCTTATACAGAAAGCGGAATTTCTGTCTGAGAGAGCTTGGTTCTACATCTGGA 661
QY      223 MetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetLeuAspArgIle 242
Db      662 ATGGAGCGGTATGACACACTGATGATCTGTCTCCCTGGCAACCATGATTGATCGAATA 721
QY      243 LysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGly 258
Db      722 AAAAGACACTTAACATCTCATTTTCCTTGGCCCTTGGGGTGGGG 769

RESULT 6
AL521920 957 bp mRNA linear EST 22-MAY-2003
LOCUS     AL521920
DEFINITION Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
CDNA clone CS0DB003YPI4 5-PRIME, mRNA sequence.
ACCESSION AL521920
VERSION   AL521920.2 GI:31040194
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 957)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE     Full-length cDNA libraries and normalization
JOURNAL   Unpublished
COMMENT   On Feb 13, 2001 this sequence version replaced g1:12785413.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1287.f. For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DB003YPI4&cluster=1287.f. Contact :
Feng Liang Email: fliang@lifetech.com url:
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0DB003H070P1.
Location/Qualifiers
    1..957
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="CS0DB003YPI4"
    /tissue_type="NEUROBLASTOMA COT 10-NORMALIZED"
    /clone_lib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
    /note="1st strand cDNA was primed with a NotI-oligo(dT)
    primer. Five prime end enriched, double-strand cDNA was
    digested with Not I and cloned into the Not I and EcoR V
    sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 250 a 239 c 217 g 250 t 1 others
ORIGIN

```

Alignment Scores:

Pred. No.: 1,79e-225 Length: 957
 Score: 243.00 Matches: 243
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 69.43% Indels: 0
 DB: 9 Gaps: 0

US-09-745-506-37 (1-350) x AL521920 (1-957)

QY 1 MetaspLeuYsAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
 DB 166 ATGGATTGGAAGGCTCCCTCTCTCTGATGACTTGTGATCCCTCTGCTGAG 225
 QY 21 SerTrpAspAsnValGlyLeuLeuValGluProSerProHisThrValAsnThrLeu 40
 DB 226 AGTTGGACAATGTGGATTACTGTGTGAACCAAGCCACCACTGTAATATACACTC 285
 QY 41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
 DB 286 TTCTGTACCAATGACCTGACTGAGAGATGATGAGAGAGTGTGCAAAAGAGGACAC 345
 QY 61 LeuLeuSerSerTrpHisProPheArgPheArgProMetLysArgLleThrTrpAsnThr 80
 DB 346 CTGATTCTCTCTACCACTCCGCTATCTTCGACCACTGAAAGCCCACTGAGACACA 405
 QY 81 TrpLysGluArgLeuValLleArgAlaLeuGluAsnArgValGlyLleTrSerProHis 100
 DB 406 TGGAAAGAGCGCCGTGGATCCGGGCTGTGAGAAACAGAGCGGTATCTCTCTCAT 465
 QY 101 ThrAlaTrpAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
 DB 466 ACAGCCTATGATGTGGGCGCCAGGCGGTCAACAACTGTGGCTAAAGGCTTGAGCT 525
 QY 121 CysThrSerArgProLleHisProSerLysAlaProAsnTrpProThrGluGlyAsnHis 140
 DB 526 TGTACTCTCCAGCCCATATCATCTCTCCAAAGCTCCCACTACCTACAGAGAGAAACAC 585
 QY 141 ArgValGluPheAsnValAsnTrpThrGlnAspLeuAspLysValMetSerAlaValLys 160
 DB 586 CGAGTAGAATTCACAGTTACTACACCAACCGGACAAAGTCATCTGCAAGTGAAA 645
 QY 161 GlyLleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluThr 180
 DB 646 GGAATGACGGTGTCTCTGTCACCTCTTTCTGCTAGACTGCTAATGAGACAAACA 705
 QY 181 ArgLleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArg 200
 DB 706 CGGATTATATCGAATTTGTAACAGAAAGCTTTGATGCGATGATTTCTTCCCGG 765
 QY 201 AsnLysGlnLeuTrpGlnLysThrGluLeuSerLeuGluLysProLeuLeuHis 220
 DB 766 AACCAAAACACTTATACAGAAAGCGAAATTCGTCACTGAGAGAACCTTTGCTTCAAT 825
 QY 221 ThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetLleAsp 240
 DB 826 ACTGGAATGGAGCGGTATGCACTGATGATATCTGCTCCCTGCAACCATGATGAT 885
 QY 241 ArgLleLys 243
 DB 886 CGAATATAA 894
 RESULT 7
 LOCUS BM545164 1117 bp mRNA linear EST 20-FEB-2002
 DEFINITION AGENCOURT_6497454 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5588980
 ACCESSION BM545164
 VERSION BM545164.1 GI:18777026
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1117)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps@email.nih.gov
 Tissue Procurement: Invitrogen
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: L14M12360 row: p column: 05
 Location/Qualifiers
 1. 1117

FEATURES

source
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5588980"
 /lab_host="DH10B"
 /clone_11b="NIH_MGC_125"
 /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
 Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool
 of three ovaries, from females ranging in age from 38 to
 49 yo. Library is oligo-dT primed and directionally cloned
 (EcoRV site is destroyed upon cloning). Average insert
 size 2.1 kb, insert size range 1-3.5 kb. Library is
 normalized and enriched for full-length clones and was
 constructed by C. Gruber (Invitrogen). Research Genetics
 tracking code 036."
 BASE COUNT 278 a 282 c 260 g 293 t 4 others
 ORIGIN

Alignment Scores:

Pred. No.: 1.98e-224 Length: 1117
 Score: 242.00 Matches: 242
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 69.14% Indels: 0
 DB: 12 Gaps: 0

US-09-745-506-37 (1-350) x BM545164 (1-1117)

QY 1 MetaspLeuYsAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
 DB 88 ATGGATTGGAAGGCTCCCTCTCTCTGATGACTTGTGATCCCTCTGCTGAG 147
 QY 21 SerTrpAspAsnValGlyLeuLeuValGluProSerProHisThrValAsnThrLeu 40
 DB 148 AGTTGGACAATGTGGATTACTGTGTGAACCAAGCCACCACTGTAATATACACTC 207
 QY 41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
 DB 208 TTCTGTACCAATGACCTGACTGAGAGATGATGAGAGAGTGTGCAAAAGAGGACAC 267
 QY 61 LeuLeuSerSerTrpHisProPheArgPheArgProMetLysArgLleThrTrpAsnThr 80
 DB 268 CTGATTCTCTCTACCACTCCGCTATCTTCGACCACTGAAAGCCCACTGAGACACA 327
 QY 81 TrpLysGluArgLeuValLleArgAlaLeuGluAsnArgValGlyLleTrSerProHis 100
 DB 328 TGGAAAGAGCGCCGTGGATCCGGGCTGTGAGAAACAGAGCGGTATCTCTCTCAT 387
 QY 101 ThrAlaTrpAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
 DB 388 ACAGCCTATGATGTGGGCGCCAGGCGGTCAACAACTGTGGCTTAAAGGCTTGAGCT 447
 QY 121 CysThrSerArgProLleHisProSerLysAlaProAsnTrpProThrGluGlyAsnHis 140
 DB 448 TGTACTCCAGGCCCATATCTCTTCAAAAGCTCCCACTACCTACAGAGAGAAACAC 507

QY 141 ArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLys 160
|||||
Db CGAGTAGAATTCACAGTTACTACACACCAGACCTGCAAGATCTGCTGACAGTAA 567
QY 161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGlnThr 180
|||||
Db GGAATTGACGGTGTCT 627
QY 181 ArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArg 200
|||||
Db CGGATTAATCTCAATTTGATCTCAGAGAGCGCTTGATGACGATGATTTCTTCCCG 687
QY 201 AsnLysGlnLeuTyrGlnLysThrGlnLeuSerLeuGluLysProLeuLeuHis 220
|||||
Db AACAAACAACCTTATCAGAGACGAAATTTCTGCTCAGAGAGCTTTGCTTCTACT 747
QY 221 ThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAsp 240
|||||
Db ACTGGAATGGACGGTTATGACACTGATGATGATGCTCTCCCTGGCAACCATGATGAT 807
QY 241 ArgIle 242
|||||
Db 808 CGAATA 813
RESULT 8
AL520538 890 bp mRNA linear EST 22-MAY-2003
LOCUS AL520538 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
DEFINITION CDNA clone CS0DB006Y18 5-PRIME, mRNA sequence.
ACCESSION AL520538
VERSION AL520538.2 GI:31038879
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 890)
L1, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12784031.
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr
Library was constructed by life technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1287.f for
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DB006DC090Plac1cluster=1287.f. Contact :
Peng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DB006DC090Pl.
FEATURES
source
1..890
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DB006Y18"
/tissue_type="NEUROBLASTOMA COT 10-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-poly(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 230 a 224 c 201 g 234 t
ORIGIN
Alignment Scores:
Pred. No.: 1,12e-219 Length: 890
Score: 237.00 Matches: 237
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 67.71% Indels: 0
DB: 9 Gaps: 0
US-09-745-506-37 (1-350) x AL520538 (1-890)
QY 1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
|||||
Db ATGAGATTAAAGGCT 237
QY 21 SerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
|||||
Db AGTTGGGCAAAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 297
QY 41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuLeuLysLysAlaAsp 60
|||||
Db TTCCCGACCAACATGACCTGACTGAGGAGATGAGAGAGTGTGCAAAARAAAGGAGAC 357
QY 61 LeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTrpAsnThr 80
|||||
Db CTCATCT 417
QY 81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
|||||
Db TGAAGAGACCGCGCTGTGATCCGGCTGTGAGAACAGAGTGGTATCTACTCTCTCAT 477
QY 101 ThrAlaTyrAspAlaAlaProGlnGlyValAsnAspTrpLeuAlaLysGlyLeuGlyAla 120
|||||
Db 478 ACAGCCTATGATGCTGCGCCCGCCAGGGCGTCAACACTGGTTGGCTTAAAGGCTTGAAGCT 537
QY 121 CysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHis 140
|||||
Db 538 TGTACTCTCCAGGCCCTATATCT 597
QY 141 ArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLys 160
|||||
Db 598 CGAGTAGAATTCACAGTTACTACACACCAGACCTGCAAGATGATGCTGCTGACAGTAA 657
QY 161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGlnThr 180
|||||
Db 658 GGAATTGACGGTGTCT 717
QY 181 ArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArg 200
|||||
Db 718 CGGATTAATCTCAATTTGATCTCAGAGAGCGCTTGATGACGATGATTTCTTCCCG 777
QY 201 AsnLysGlnLeuTyrGlnLysThrGlnLeuSerLeuGluLysProLeuLeuHis 220
|||||
Db 778 AACAAACAACCTTATCAGAGACGAAATTTCTGCTCAGAGAGCTTTGCTTCTACT 837
QY 221 ThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThr 237
|||||
Db 838 ACTGGAATGGACGGTTATGACACTGATGATGATGCTCTCCCTGGCAAC 888
RESULT 9
BM557530 1019 bp mRNA linear EST 20-FEB-2002
LOCUS BM557530
DEFINITION AGENCOURT_6563433 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5739935
5', mRNA sequence.
ACCESSION BM557530
VERSION BM557530.1 GI:18799594
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1019)
NIH-MGC http://mhc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>

Plate: L1M12734 row: a column: 24
 High quality sequence stop: 685.
 Location/Qualifiers

FEATURES

source

1. 1019
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:573935"
 /tissue_type="duodenal adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH-MGC-88"
 /note="Organ: small intestine; Vector: pCMV-SPORT6;
 Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
 oligo-qt primed. Average insert size 1.767 kb. Library
 enriched for full-length clones and constructed by Life
 Technologies. Note: this is a NIH-MGC Library."

BASE COUNT 256 a 254 c 236 g 271 t 2 others
 ORIGIN

Alignment Scores:

Pred. No.: 4.64e-204 Length: 1019
 Score: 221.00 Matches: 221
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 63.14% Indels: 0
 DB: 12 Gaps: 0

US-09-745-506-37 (1-350) x BM557530 (1-1019)

Qy 1 MetaspLeuYrAlaLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
 Db 107 ATGGATTGAAAGGCGCTCTTCTTCTGATGCTTTCATCCCTCGTTGCTAG 166
 Qy 21 SerTPAspaanValGlyLeuLeuValGluProSerProPHisthValAsnThrLeu 40
 Db 167 AGTGGGAGCATGTTGGATTACTGCTGAGACCAAGCCACACATACCTGAATACACTC 226
 Qy 41 PheLeuThrAsnAspLeuThrGluGluValMetGluValLeuGluLysAlaAsp 60
 Db 227 TTCTCTGACCAATGACTCTACTGAGAGAGTGTGAGGTGCTGCAAAAGGCAACAC 286
 Qy 61 LeuLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTyrAsnThr 80
 Db 287 CTCATTCTCTTACCATCCGCTATCTTCCGACCCATGAAGCGCATTAACCTGGAAACA 346
 Qy 81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
 Db 347 TGGAAAGAGCGCGCTGATATCCGGGCTCGAGAAACAGATCGGATCTACTCTCTCAT 406
 Qy 101 ThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
 Db 407 ACAGCGTATGATGCGCGCCAGGCGCTCAACAACATGTTGGCTAAAGGCGTTGAGACT 466
 Qy 121 CysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHis 140
 Db 467 TGTACTCTCAGGCGCCATCATCTTCCCAAGCTCCCAACTCCCACTACAGAGGAAACAC 526
 Qy 141 ArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLys 160
 Db 527 CGAGTGAATTCACAGCTTAACATACCAAGACCTGGAGCAAGTATATGTCTGCACTGAAA 586
 Qy 161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluInThr 180
 Db 587 GGAATTTAGAGGTTTCTGTCACTCTTTCTCTGTAGACCTGGTAATGAGAGCAACAACA 646
 Qy 181 ArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArg 200

Db 647 CGGATTATCTGAATTTACTCAGAGGCTTTGATGAGGTGATTTTCTTCCCG 706
 Qy 201 AsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuHis 220
 Db 707 AACAAACAACTTATTCAGAAAGACGGAATTTCTGACTGAGAGGCTTTGCTTACAT 766

Qy 221 Thr 221
 Db 767 ACT 769

RESULT 10

AL529615 1201 bp mRNA linear EST 23-MAY-2003
 LOCUS AL529615 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
 DEFINITION cDNA clone CS0DD006D06YH18 5-PRIME, mRNA sequence.

ACCESSION AL529615
 VERSION AL529615.2 GI:31067458
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

REFERENCE
 AUTHORS L.M.B., Gruber,C., Jesse,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT On Feb 13, 2001 this sequence version replaced gi:12793108.

CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 1287.f For more information about this cluster, see
[http://www.genoscope.cns.fr/](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DD006D06D09QP1&cluster=1287.f)
 Feng Liang Email: fliang@lifestech.com URL: <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID: CS0DD006D09QP1.

FEATURES

source

1. 1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DD006YH18"
 /tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
 /clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 319 a 286 c 274 g 299 t 23 others
 ORIGIN

Alignment Scores:

Pred. No.: 4.01e-199 Length: 1201
 Score: 216.00 Matches: 268
 Percent Similarity: 99.26% Conservative: 0
 Best Local Similarity: 99.26% Mismatches: 1
 Query Match: 61.71% Indels: 2
 DB: 9 Gaps: 0

US-09-745-506-37 (1-350) x AL529615 (1-1201)

Qy 23 AspaanValGlyLeuLeuValGluProSerProPHisthValAsnThrLeuPheLeu 42
 Db 237 GACATGTTGATTTACTGCTGGAACCAAGCCACCATCTATGTAATACACTTCTCTG 296
 Qy 43 ThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysAlaAspLeuIle 62
 Db 297 ACCAATGACCTGACGAGAGAGTGTGAGAGGTGCTGCAAAAGAGCAGACCTCATY 356
 Qy 63 LeuSerTyrHisProProIlePheArgProMetLysArgIleThrTyrAsnThrTyrLys 82

|||||
Db 357 CTTCTCTACCAACCGGCTATCTCCGACCATGACGCGATACCTGGAACACATGAGG 416
Qy 83 GUAAGLeuVal1LeuArgAlaLeuGluAsnArgValGlyLeuSerProHisThrAla 102
Db 417 GAGCGCGTGTGTCCGGCTCTGAGAACAGAGTGTATCTCTCTCTATACAGCC 476
Qy 103 TTAAspAlaAlaProGlnGlyValAsnAsnThrPheAlaGlyLeuGlyAlaCysThr 122
Db 477 TATGATGCTGCGCCCGAGGCGTCACCAACTGCTGTGAAGGCTTGAGCTTATACC 536
Qy 123 SerArgProIleHisProSerLysAlaProAsnTyrProThrGlnGlyAsnHisArgVal 142
Db 537 TCCAGGCCCATCATCTCTCCAAAGCTCCCAACTACCTACACAGAGGAAACCCAGAT 596
Qy 143 GluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLysGlyIle 162
Db 597 GAATTCACAGCTTAACACACCCAAAGCTGAGCAAAAGTCATGTCTCAGTGAAGGAATT 656
Qy 163 AAGGlyValSerValThrSerPheSerAlaArgThrGlyAsnGlnGlnThrArgIle 182
Db 657 GACGGCTTCTGTCTCACTCTTTTCTGCTAGACACTGTAATGAGAACACACGAGATT 716
Qy 183 AsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArgAsnLys 202
Db 717 AATCTGAATTGTACTCAGAAAGCTTGATGACAGCTGTGATTTCTTCCCGAACA 776
Qy 203 GlnLeuTyrGlnLysThrGlnLysLeuSerLeuGlnLysProLeuLeuHisThrGly 222
Db 777 CAACCTTATCAGAAAGCGAAATTCGTACCTGAGAACAGCTTTGTCTTACTACTGGA 836
Qy 223 MetGlyArgLeuGlySerThrLeuAspGluSerValSerLeuAlaThrMetIle-AspArgIle 242
Db 837 ATGGGACGGTTATGACACTGATGATGTCTCTCCCTGCAACCATGAA-TGATGAAAT 895
Qy 242 eLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThrLeuGly 262
Db 896 AAAAACAACACTTAACTATCTCATATCTGCTTACGCCCTTGCGGGGAGAACCTTACA 955
Qy 262 UserGlnValLysValValAlaLeuGlyAsnGlySerGlySerSerValLeuGlnGlyVal 282
Db 956 GTCTCAAGTCAAAAGTGTGGCCCTGTGTGCGGCTCTGGAGAGCAGCTTGTGAGGGTGT 1015
Qy 282 LgluAlaAspLeuTyrLeuThrGlyGlu 291
Db 1016 TGAGGCTGACCTTACTCAGAGGTGAG 1043

RESULT 11
BQ437698 877 bp mRNA linear EST 24-MAY-2002
LOCUS AGENCOURT 7894666 NIH_MGC_72 Homo sapiens cdna clone IMAGE:6158334
DEFINITION 5', mRNA sequence.
ACCESSION BQ437698
VERSION BQ437698.1 GI:21176774
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 877)
NIH-MGC <http://mgi.ncl.nih.gov/>,
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DRP
cdna Library Preparation: Life Technologies, Inc.
cdna Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LHAM13505 row: k column: 07

FEATURES High quality sequence stop: 667.
Location/Qualifiers
source 1..877
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6158334"
/issue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-Sport6; site_1: NotI;
site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
BASE COUNT 247 a 181 c 206 g 242 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 2,51e-197 Length: 877
Score: 214.00 Matches: 214
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 61.14% Indels: 0
DB: 13 Gaps: 0
US-09-745-506-37 (1-350) x BQ437698 (1-877)
Qy 137 GUGGlyAsnHisArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMet 156
Db 26 GAGGGAACACCGAGATGAAATTCACGTTACTACACCCAAAGCTGGAAGATC 85
Qy 157 SerAlaValLysGlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsn 176
Db 86 TCTGCACTGAAGAAGATTGACGCTTCTGTCTACTTCTTTCTCTAGAGATGGAAT 145
Qy 177 GUGGlnGlnThrArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAsp 196
Db 146 GAGGAACAAACAGGATTAATCTGAATTGATTAAGCTTGAAGCTTGAAGCAGTGTGAT 205
Qy 197 PheLeuSerArgAsnLysGlnLysTyrGlnLysThrGlnLysLeuSerLeuGlyPro 216
Db 206 TTTCTTCCCGGAACAAACCTTTATCAACAAACGGAATTTGTCTACTGAGAAAGCT 265
Qy 217 LeuLeuLeuHisThrGlyMetGlyArgLeuGlySerThrLeuAspGluSerValSerLeuAla 236
Db 266 TTGCTTCTACTACTGGAATGAGGACGCTTATGCACACTGATGATGTCTCCCTGGCA 325
Qy 237 ThrMetIleAspArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGly 256
Db 326 ACCATGATGATGCAATTAACAAACACTTATCTCATATTCGCTTACGCCCTTGGG 385
Qy 257 ValGlyArgThrLeuGlnLysGlnValValAlaLeuGlyAsnGlySerGlySer 276
Db 386 GTGGGGAACCTTAGAGTCTCAAGTCAAAAGTGTGGCCCTGTGTGCTGTGGAGC 445
Qy 277 SerValLeuGlnGlyValGluAlaAspLeuTyrLeuThrGlyGlnMetSerHisAsp 296
Db 446 AGGTTCTGAGAGGTGTGAGGCTGACCTTACTCTACAGTGAAGTCCATCATGAT 505
Qy 297 ThrLeuAspAlaAsnArgGlnGlyIleAsnValIleLeuGlySerGlnHisSerAsnThrGlu 316
Db 506 ACTTTGATGCTCTTCCCAAGGAATTAAGTATCTCTCTGTGACACACAAACACTGAA 565
Qy 317 ArgGlyPheLeuSerAspLeuArgAspMetLeuAspSerHisIleGlnGluAsnLys 336
Db 566 CGAGGCTTCTTCTGTGACTTCAAGATATCTGGAATTCAGTTGGAGAAATGAATTAAT 625
Qy 337 IleIleLeuSerGluThrAspArgAspProLeuGlnValVal 350
Db 626 ATTATCTATCAGAGACTGACAGGAGACCTCTTCAGGTGTA 667

RESULT 12
B0859307

/note="Organ: skin; Vector: pORF7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACAG(G). Size selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 191 a 196 c 173 g 198 t 1 others
 ORIGIN

Alignment Scores:
 Pred. No.: 2,02e-196 Length: 759
 Score: 213.00 Matches: 213
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 60,868 Indels: 0
 DB: 10 Gaps: 0

US-09-745-506-37 (1-350) x BE275324 (1-759)

OY 1 MetAspLeuLysAlaLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
 DB 86 ATGGATTGAAAGGCTCTCTCTCTGAAATGACTTGCATCCCTCTGTTGCTGAG 145
 OY 21 SerTPAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
 DB 146 ACTTGAGACATGTTGATTACTGCTGGAACCAAGCCACACATCTGTAATATACACTC 205
 OY 41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGluInLysLysAlaAsp 60
 DB 206 TTCCTGACCAATGACTGACTGAGAAAGATGAGAGAGTGTCTGCAAAAGAGGACAGAC 265
 OY 61 LeuIleLeuSerThrHisProProIlePheArgProMetLysArgIleThrTPAsnThr 80
 DB 266 CTCATCTCTCTTACCATCGCTATCTCCGACCATGAAAGCGATACCTGGAACACA 325
 OY 81 TPryLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
 DB 326 TGAAGAGACGCGCTGATCCGCGGCTCGGAGAAAGAGTGGATCTACTCTCAT 385
 OY 101 ThrAlaTyrAspAlaAlaProGluGlyValAsnAsnTPLeuAlaLysGlyLeuGlyAla 120
 DB 386 ACAGCCTATGATGCTGCGCCAGGCGCTCAACACTGTTGGCTTAAAGGCTTGGAGCT 445
 OY 121 CysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHis 140
 DB 446 TGTACCTCCAGGCGCATACATCTTCCAAAGCTCCCACTACCTACAGAGGAAACAC 505
 OY 141 ArgValGluPheAsnValAsnTyrThrGluAspLeuAspLysValMetSerAlaValLys 160
 DB 506 CGAGTATGATTCACACTTACATACACCAAGACTGACAAAGTCTGTCAGAGTGA 565
 OY 161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluInThr 180
 DB 566 GGAATGAGCGGTCTCTCACTCTTTCTTCTGTAAGACGTGATAGGAACAACA 625
 OY 181 ArgIleAsnLeuAsnLysThrGluLysAlaLeuMetGluValValAspPheLeuSerArg 200
 DB 626 CGGATTAATCTGAATGTACTCAGAAAGGCTTGTATCAGGTGATATTTCTTCCCG 685
 OY 201 AsnLysGluLeuTyrGluLysThrGluIleLeuSerLeu 213
 DB 686 AACAAACAACTTATCAGAAAGGAAATTCGTCACTG 724

RESULT 14
 B1755123 817 bp mRNA linear EST 25-SEP-2001
 LOCUS B1755123 603022837F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5193320 5',
 DEFINITION mRNA sequence.
 ACCESSION B1755123
 VERSION B1755123.1 GI:15746701
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 817)
 AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLNL1483 row: j column: 09
 High quality sequence start: 3
 High quality sequence stop: 815.
 Location/Qualifiers

FEATURES
 source
 1..817
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5193320"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_114"
 /note="Organ: Brain; Vector: pCMV-Sport6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb. Insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH-MGC Library."

BASE COUNT 205 a 211 c 183 g 218 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1.92e-194 Length: 817
 Score: 211.00 Matches: 224
 Percent Similarity: 99.56% Conservative: 0
 Best Local Similarity: 99.56% Mismatches: 0
 Query Match: 60,29% Indels: 1
 DB: 12 Gaps: 0

US-09-745-506-37 (1-350) x B1755123 (1-817)

OY 1 MetAspLeuLysAlaLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
 DB 109 ATGGATTGAAAGGCTCTCTCTCTGAAATGACTTGCATCCCTCTGTTGCTGAG 168
 OY 21 SerTPAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
 DB 169 AGTTGGACAAITTTGATTACTGCTGGAACCAAGCCACACATCTGTAATATACACTC 228
 OY 41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGluInLysLysAlaAsp 60
 DB 229 TTCCTGACCAATGACTGACTGAGAAAGATGAGAGAGTGTGCAAAAGAGGACAGAC 288
 OY 61 LeuIleLeuSerThrHisProProIlePheArgProMetLysArgIleThrTPAsnThr 80
 DB 289 CTCATCTCTCCATACATCGCTATCTCCGACCATGAAAGCGCATTAACCTGGAACACA 348
 OY 81 TPryLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
 DB 349 TGAAGAGCGCGCTGATCCGCGCTCTGGAACACAGACTCGTATCTACTCTCAT 408
 OY 101 ThrAlaTyrAspAlaAlaProGluGlyValAsnAsnTPLeuAlaLysGlyLeuGlyAla 120
 DB 409 ACAGCCTATGATCTGCGCCAGGCGCTCAACACTGTTGGCTTAAAGGCTTGGAGCT 468

QY 121 CysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHis 140
 DB 469 TGTACCTCCAGGCCCATATCATCTTCCAAAGCTCCCAACTACCTACAGAGGAACAC 528
 QY 141 ArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLys 160
 DB 529 CGACTAGAAATTCACAGTTAACTACACCCAGACCTGGCAAGATCATGTCTGCAGTGA 588
 QY 161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluThr 180
 DB 589 GGAATTGACGGTGTCTTCTGACTCTTTTCTGCTAGAGACTGGTAATGAGGAACAA 648
 QY 181 ArgIle-AsnLeuAsnCysThrGlnLysAlaLeuMetGlnValAlaAspPheLeuSer 200
 DB 649 CGAATTATATCTGAATGTACTACAGAAAGCTTGTGATGAGGTGAGATTTTCTTCCG 708
 QY 200 GAsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuHis 220
 DB 709 GAACAACACACTTATATCAGAGAGCAAAATCTGCTACTGAGAAAGACCTTGTCTTCA 768
 QY 220 sThrGlyMetGly 224
 DB 769 TACTGGAATGGGA 781

RESULT 15
 BX377118/c 1201 bp mRNA linear EST 08-MAY-2003
 LOCUS BX377118 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 DEFINITION clone CS0D1002YM20 3-PRIME, mRNA sequence.
 ACCESSION BX377118
 VERSION BX377118.1 GI:30448573

SOURCE EST.
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1201)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 1287.f for
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0D1002BG10NP1&cluster=1287.f. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/Invitrogen 1600
 Faraday Avenue Genoscope sequence ID : CS0D1002BG10NP1.

FEATURES
 source Location/Qualifiers
 1..1201

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1002YM20"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 319 a 250 c 257 g 325 t 50 others
 ORIGIN

Alignment Scores: 2.72e-193 Length: 1201
 Pred. No.: 210.00 Matches: 223
 Score: 99.55% Conservative: 0
 Percent Similarity: 99.55% Mismatches: 0
 Best Local Similarity:

Query Match: 60.00% Indels: 1
 DB: 13 Gaps: 0
 US-09-745-506-37 (1-350) x BX377118 (1-1201)

QY 125 ProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHisArgValGluPhe 144
 DB 913 CCCATACATCTCTTCCAAAGCTCCCACTACCTACAGAGGGAACCAACCGATGAAATTC 854
 QY 145 AsnValAsnTyrThrGln-AspLeuAspLysValMetSerAlaValLysGlyIleAspGly 164
 DB 853 AACGTTAACTACACCAAGAGCTGGACAAAGTATATCTGCTAGTGAAGAAATGACGG 794
 QY 164 ValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGlnThrArgIleAsnLe 184
 DB 793 TGTTCGTGCTACTCTTTTCTGCTAGAACTGTAAGAGGAAACACAGCATTAATCT 734
 QY 184 uAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArgAsnLysGluLe 204
 DB 733 GAATTTGATCTAGAAAGCTTGTGATGAGGTGATGATTTTCTTCCCGGAACAAACAAT 674
 QY 204 uTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuHisThrGlyMetGly 224
 DB 673 TTATCAGAAAGACGGAATTTCTGCTACGTGAGAAAGCTTGTCTACATACCTGGAATGG 614
 QY 224 YArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAspArgIleLysArg 244
 DB 613 ACGTTATGACACACTGATGATGATGTCCTCGCAACATGATGATGATGATGATGATGAT 554
 QY 244 GHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThrLeuGluSerGly 264
 DB 553 ACACCTAAACTATCTCATATTCGCTTATGCGCTTGGGGTGGGGAACCTTAGAGTCTCA 494
 QY 264 nValLysValAlaLeuCysAlaGlySerGlySerSerValLeuGlnGlyValGluAl 284
 DB 493 AGTCAAATCTCGTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 434
 QY 284 aAspLeuTyrLeuThrGlyGluMetSerHisAspThrLeuAspAlaIleSerGlnGly 304
 DB 433 TGACCTTAACTCACAGGTGAGATGTCCTCATCATGATGATGATGATGATGATGATGATG 374
 QY 304 YIleAsnValIleLeuCysGluHisSerAsnThrGluArgIlePheLeuSerAspLeuArg 324
 DB 373 AATAAATCTATCCCTGTGAAACACAGACACGAAAGAGAGCTTTCTTCTGACCTTCG 314
 QY 324 GAspMetLeuAspSerHisLeuGluAsnLysIleAsnIleLeuSerGluTyrAspArg 344
 DB 313 AGATATGCTGATTTCTCATCTTGAGAAATGATTAATATTTATCTATCAGAGACTGACAG 254
 QY 344 GAspProLeu 347
 DB 253 GGACCTCTTN 244

Search completed: August 23, 2003, 22:13:46
 Job time : 1904 secs